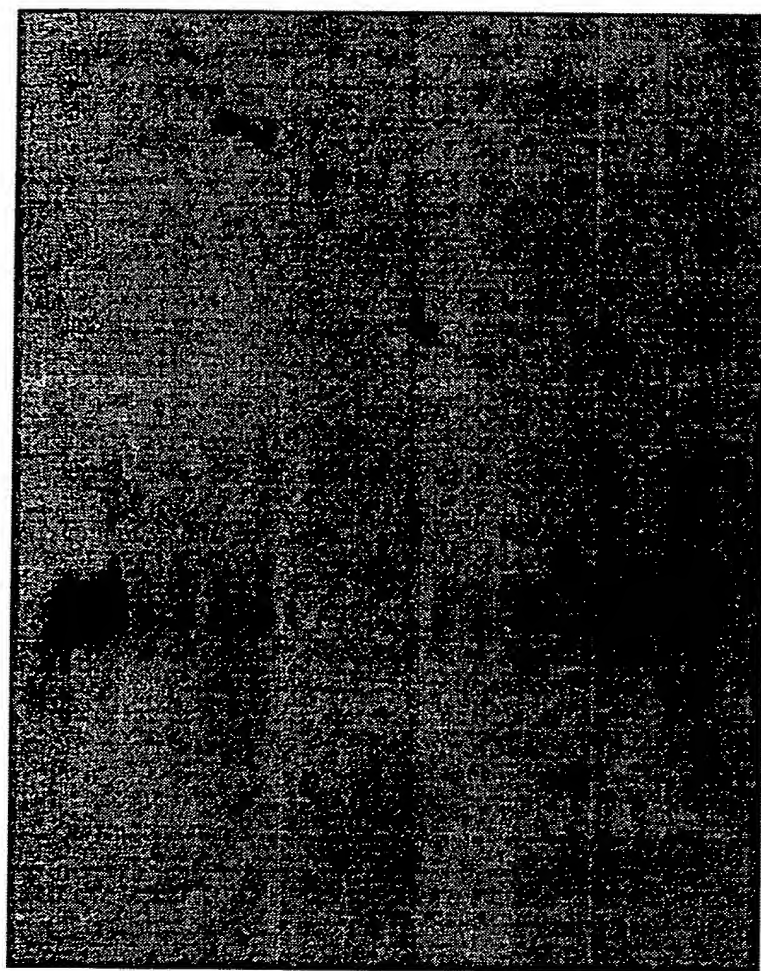


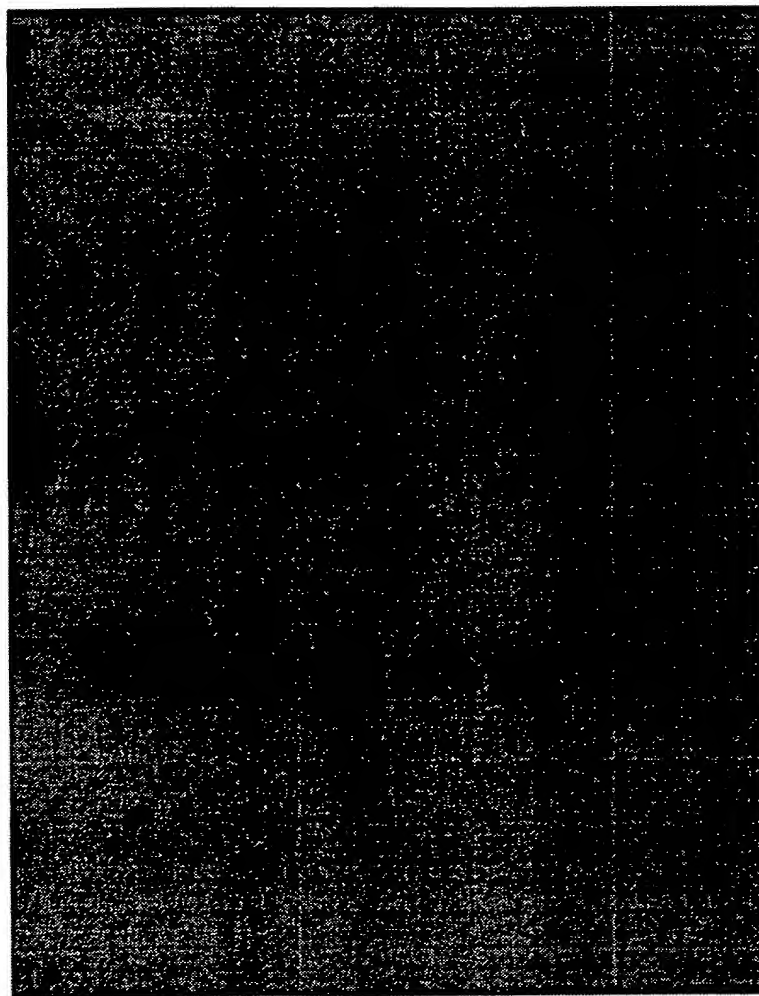
09/403861.021100



- 28S

- 18S

Fig. 1A



- 28S

- 18S

Fig. 1B

001120 19850460

1 CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGTCACTTC
 53 TCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCACTGCAGCCTACTCCT
 113 TGCTTCAGGGCCTGACTGCAACGCCAAAGCCTATCCTATAGCGGCAGCGCCAGCAGCCAC
 173 TCAAACCAGCCACAGCTCCCCGGCAACCGAACCATGAACACCGAAATGTATCAGACCCCC
 MetAsnThrGluMetTyrGlnThrPro
 233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTTCTCCACCTCCTTCTTTTCTTCTCTGCTT
 MetGluValAlaValTyrGlnLeuHisAsnPheSerThrSerPhePheSerSerLeuLeu
 293 GGAGGGGATGTGGTTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC
 GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla
 353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG
 LeuAspAsnLysIleGluGlnAlaMetAspLeuValLysAsnHisLeuMetTyrAlaVal
 413 AGAGAGGAGGTGGAGGTCCTBAAGGAGCAGATTTCGTGAGCTGCTTGAGAAGAACTCCCAG
 ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln
 473 CTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC
 LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe
 533 CAGTCCCGGCTGAGCCCTGAAGAGCCAGCACCTGAAGCCCCAGAAACCCCGGAAACCCCG
 GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrPro
 593 GAAGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCTTAGGGTGGGCAGAGCCACAT
 GluAlaProGlyGlySerAlaVal *
 653 CTTGTTCTACCTAGTTCTTTCCAGTTTGTGTTTTGGCTCCCCAAGGGTCATCTCATGTGGA
 713 GAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCAAGGACATGCCCATCTGGGT
 773 CCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCTGGAGACTAAGTTGCATGGGGC
 833 CTAGTAACACCAAGCCAGTGAGCCTGTCGTGTACCGGGCCCTGGGGGCTCCCAGGGCTG
 893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCT
 953 CCAGAAAAGTGTAAAGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCTGA
 1013 CAATGACTGTTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAACCTCTCTCTTCT
 1073 TCCTCTGTCTTTTCCAGGCAGGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTG
 1113 TTGGTTAATACTGTATAATGCATGGCTTTGTGTCACAGCCAGTGTGGGGTTACAGCTTTG
 1193 GGATGACTGCTTATAAAGTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT
 1253 AATGCGTATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACATATA
 1313 CACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACTGACTGGTCTCTTAT
 1373 CTCTTAAAGCTAAGTTTTTGAAGTGTGCTAATTTACCAAATTGATCCAGTTTGTCTTTAG
 1433 ATTAAATAAGACTCGATATGAGGGAGGGAGGGGAAGACCAGCCTCACAATGCGGGCCACAG
 1493 ATGCCTTGCTGCTGCAGTCCTCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGA
 1553 ATGCCAAACCCACCATTTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAGATCAGT
 1613 TTGGACTTCACATTTTTGTTTTAAGTTTTAGGTTGTTTTTTTTTGGTTTTGTTTGTGTTGT
 1673 TTGTTTGTGTTTTTGTGTTTTTGTGTTTTTCTTTTTTAAGTTCTTGTGGGGAACTTTGGG
 1733 GTTAATCAAAGGATGTAGTCTGTGGTAGACCAGAGGAGTAAGTACTAGTTTGTATCCTTTGG
 1793 GGTGTGGAATAATGTACCCAGGAAGCTTGTGTAAGGAGGTTCTGTGACAGTGAACACTTTC
 1853 CACTTTCTGACACCTCATCTGTGTACGACTCCAGGATTGGAATTTGGAATTTTCAAAT
 1913 GTAGCTTGAAATTTCAATAAACTTTGCTCCTTTTTCTAAAAATAAAAAAAAAAAAAAAAAA

Fig. 2

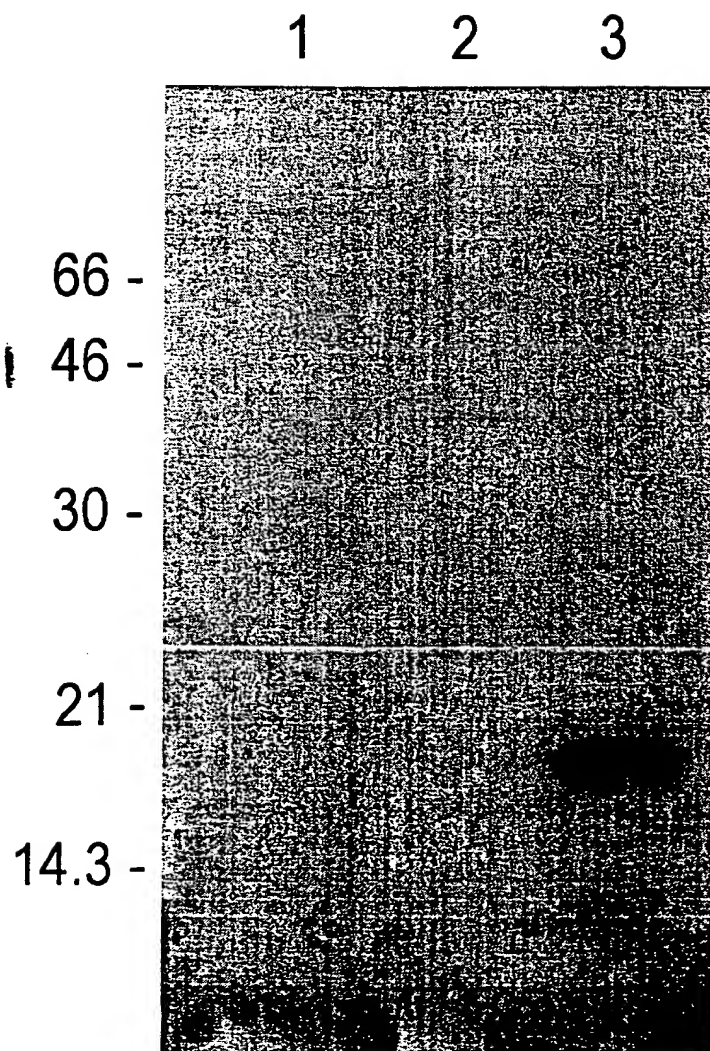


Fig. 3A

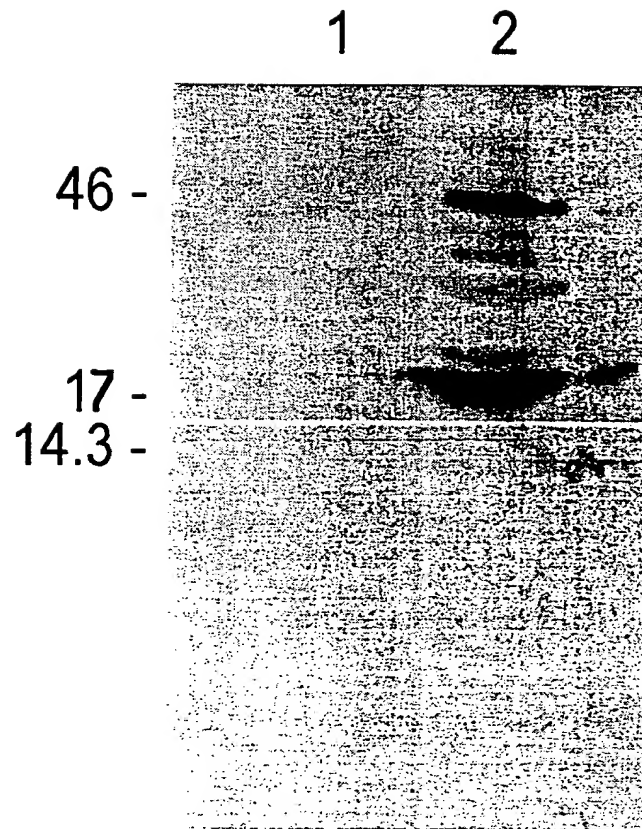


Fig. 3B

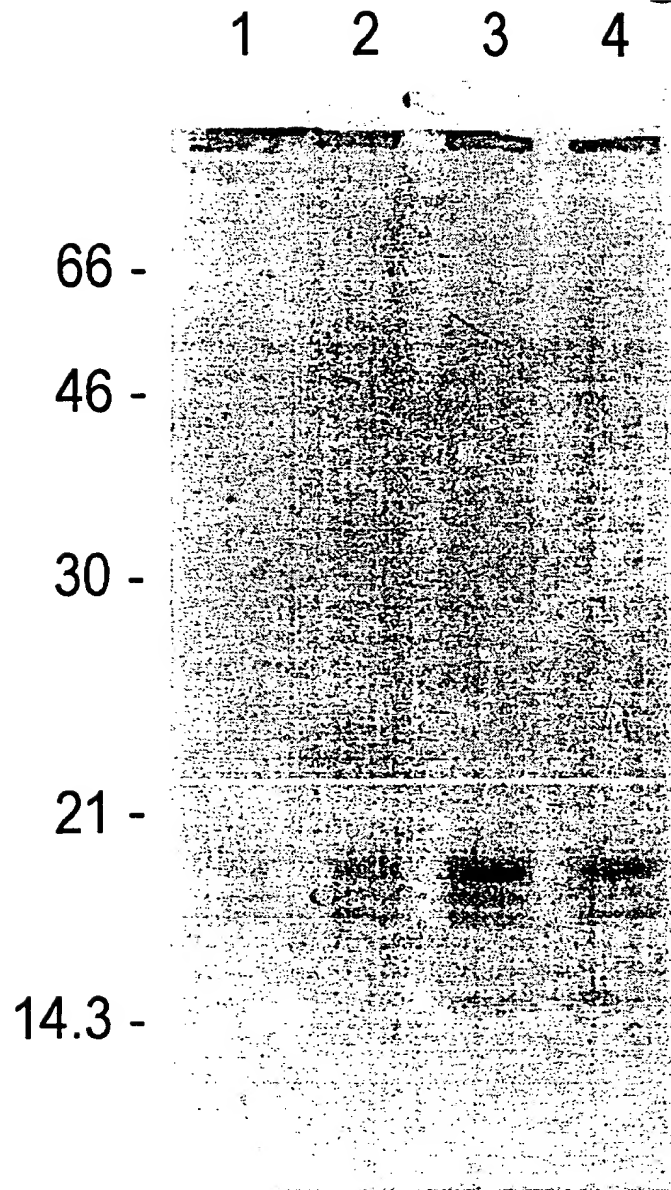


Fig. 3C

001120 19950460

GILR	L	K	E	Q	I	R	E	L	L	E	K	N	S	Q	L	E	R	E	N	T	L	L	K	T	L	A
TSC-22	L	K	E	Q	I	K	E	L	I	E	K	N	S	Q	L	E	Q	E	N	D	L	L	K	T	L	A
GCN4	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L	V
CREB	L	E	N	R	V	A	V	L	E	N	Q	N	K	T	L	I	E	E	L	K	A	L	K	D	L	Y
CREM	L	E	N	R	V	A	V	L	E	N	Q	N	K	T	L	I	E	E	L	K	A	L	K	D	L	Y
c-jun	L	E	E	K	V	K	T	L	K	A	Q	N	S	E	L	A	S	T	A	N	M	L	R	E	Q	V

Fig. 4

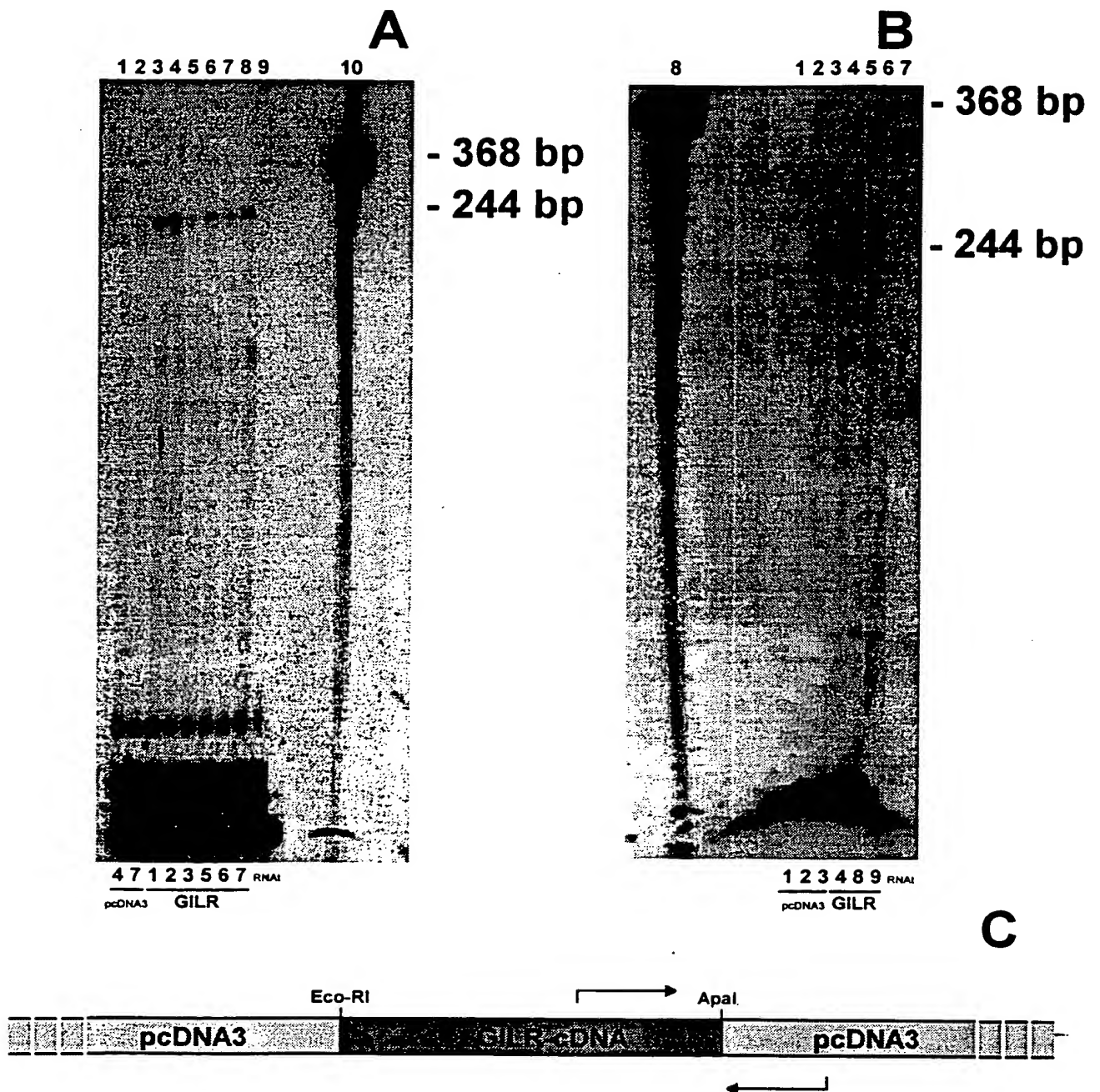


Fig. 5

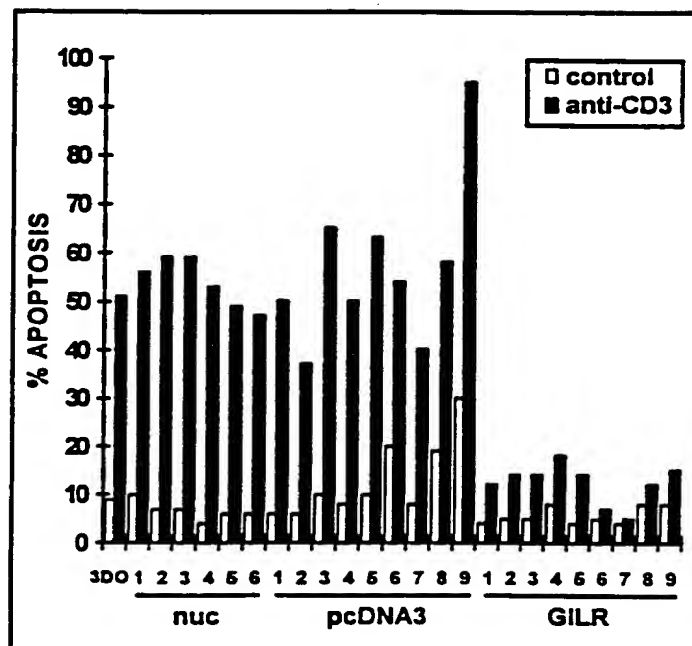


Fig. 6

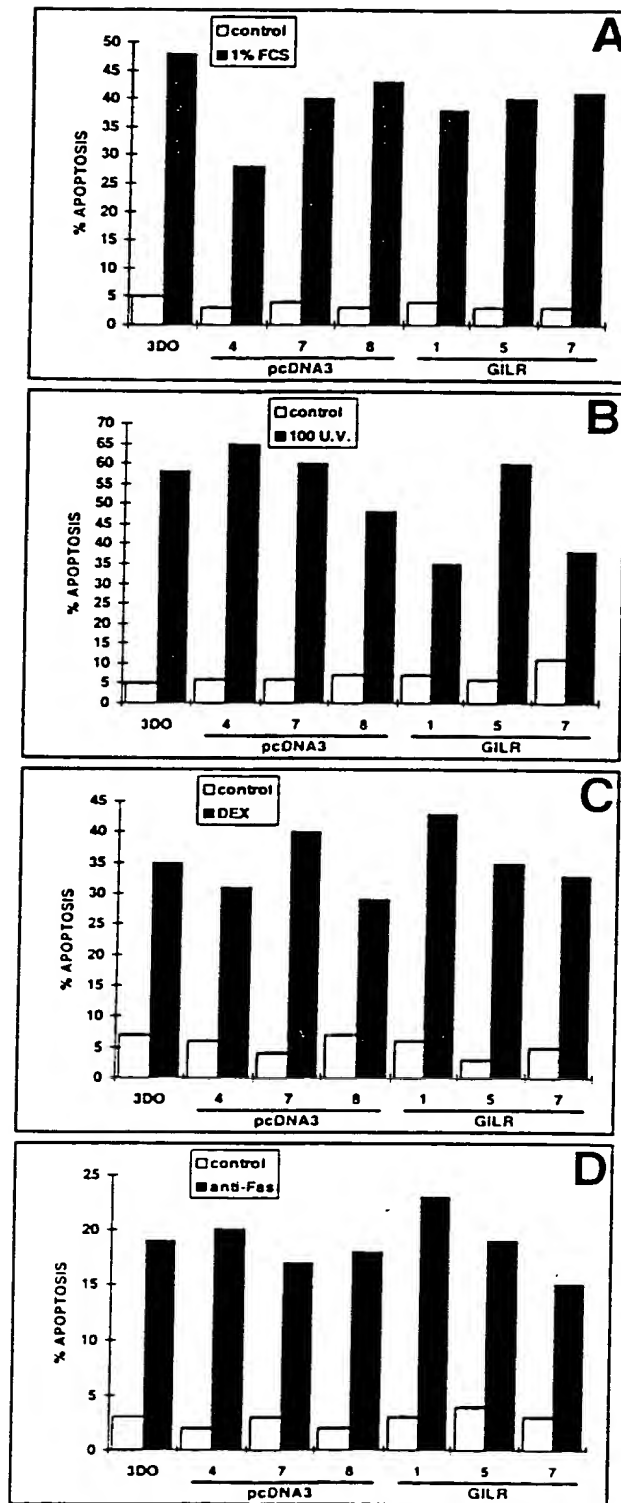


Fig. 7

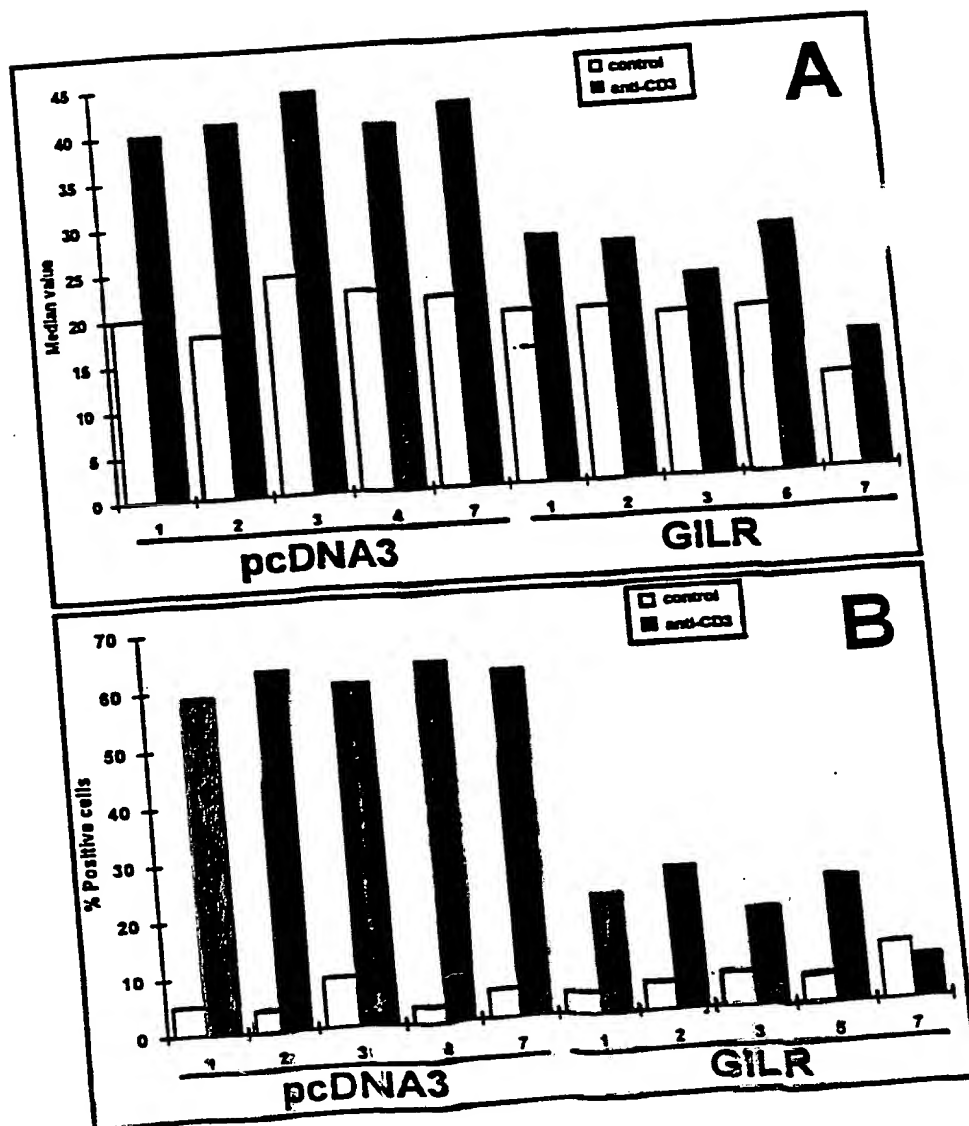
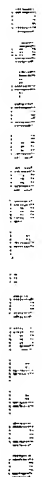


Fig. 3



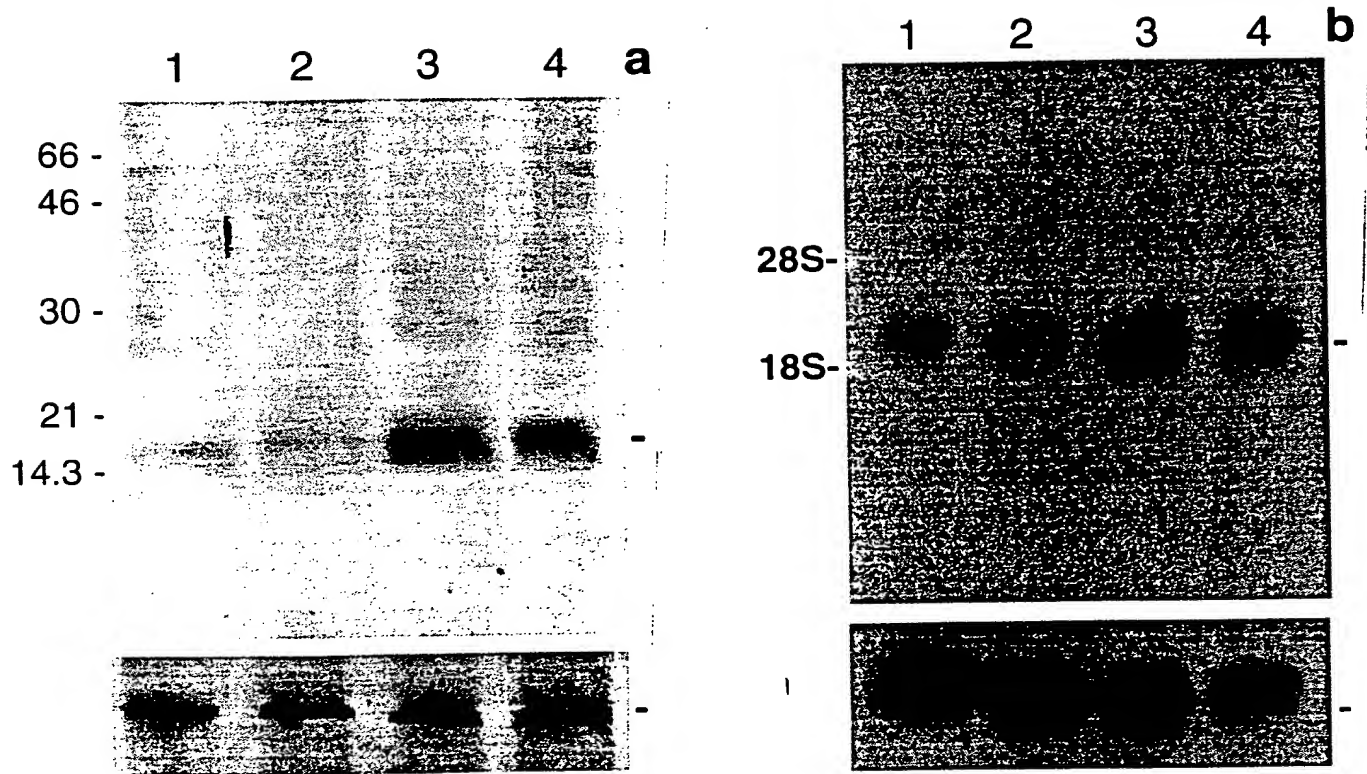


Fig. 11

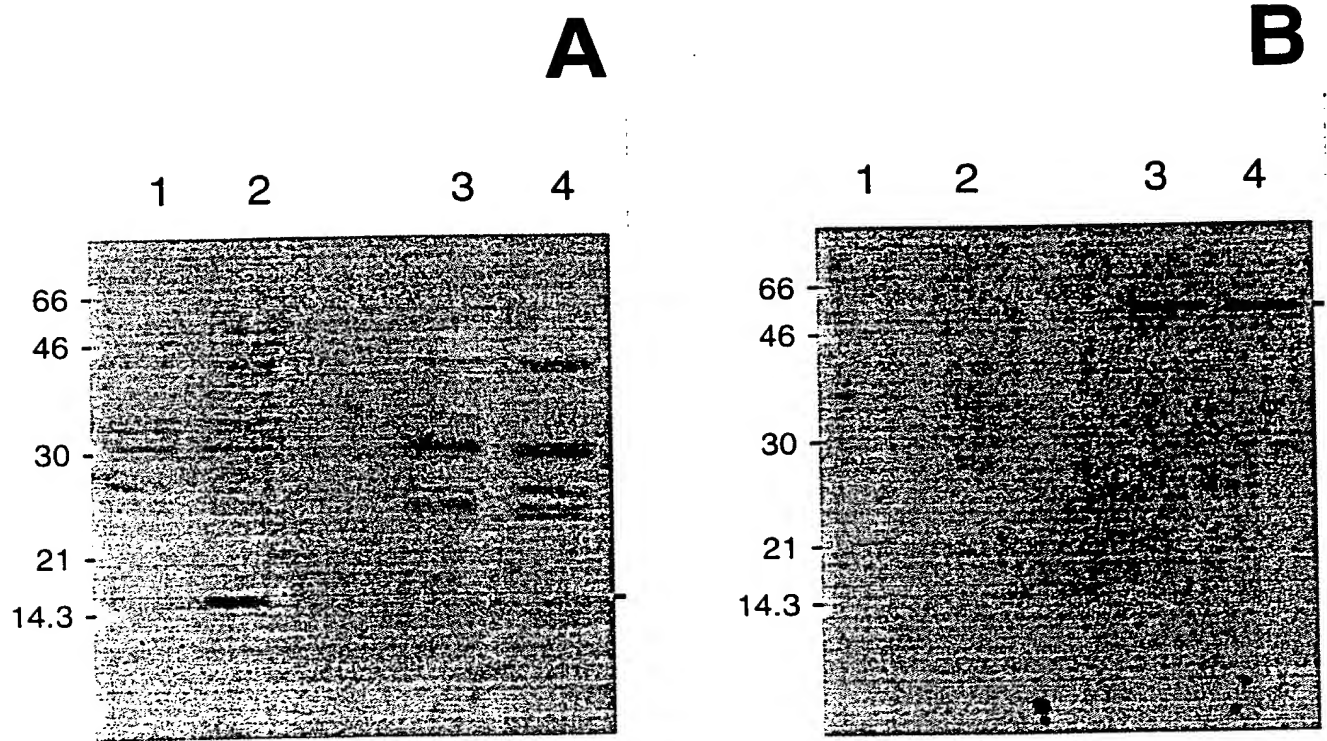


Fig. 12

1 AATTCGGGGGCGTGGAGTTTGTGACATACGAGGTGACACCCCTCGAGTCACTTCCCTTC
 61 AACTCCAGCTGGAGCGCCTGCTTGGCTTTGGGTTTCGTTCTGCAGCCTTCGCCCCGCTCCT
 121 AGCCTCAGGGCCGGACTCCAGCGCAGAGCCCAGCCAGCGCAGCCTGCCAGCAGCCACCC
 181 AGCCGCCAGCCGCCAGCCCCGACGAAACCCGGCCAGAGCTTCCTAGCAGCCCGAGCC
 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
 MetAsnThrGluMetTyrGlnThrProMetGluValAlaValTyrGlnLeuHisAsnPhe

 301 TCCATCTCCTTCTTCTCTCTCTGCTTGGAGGGGATGTGGTTTCCGTTAAGCTGGACAAC
 SerIleSerPhePheSerSerLeuLeuGlyGlyAspValValSerValLysLeuAspAsn

 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAACAAGATCGAACAGGCCATGGATCTG
 SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu

 421 GTGAAGAATCATCTGATGTATGCTGTGAGAGAGGAGGTGGAGATCCTGAAGGAGCAGATC
 ValLysAsnHisLeuMetTyrAlaValArgGluGluValGluIleLeuLysGluGlnIle

 481 CGAGAGCTGGTGGAGAAGAAGTCCCAGCTAGAGCGTGAGAACACCCTGTTGAAGACCCCTG
 ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu

 541 GCAA~~C~~CCCAGAGCAGCTGGAGAAGTTCAGTCTGTCTGAGCCCTGAAGAGCCAGCTCCC
 AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro

 601 GAATCCCCACAAGTGCCCCAGGCCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCTCTCA
 GluSerProGlnValProGluAlaProGlyGlySerAlaVal *

 661 GGGTGGGCAGAGCCACTAACTTGTTTTACCTAGTTCTTTCCAGTTTGTTTTTTGGCTCCC
 721 CAAGCATCATCTCACGAGGAGAAGTTTACACCTAGCACAGCTGGTGCCAAGAGATGTCCT
 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
 841 AGGCTGAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAATGCTACTGCGCC
 901 CTGGGGGCTCCCAGGGCCTGGGCAACTTAGCTGCAACTGGCAAAGGAGAAGGGTAGTTTG
 961 AGGTGTGACACCAGTTTGCTCCAGAAAGTTTAAGGGGTCTGTTTCTCATCTCCATGGACA
 1021 TCTTCAACAGCTTCACCTGACAACGACTGTTTCCTATGAAGAAGCCACTTGTGTTTTAAGC
 1081 AGAGGCAACCTCTCTTCTCCTCTGTTTCGTGAAGGCAGGGGACACAGATGGGAGAGAT
 1141 TGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGTATAATGCATGGCTTTGTGCACAGCCC
 1201 AGTGTGGGATTACAGCTTTGGGATGACCGCTTACAAAGTCTGTTTGGTTAGTATTGGCA
 1261 TAGTTTTTCTATATAGCCATAAATGCGTATATATACCCATAGGGCTAGATCTGTATCTTA
 1321 GTGTAGCGATGTATACATATACACATCCACCTACATGTTGAAGGGCCTAACCAGCCTTGG
 1381 GAGTATTGACTGGTCCCTTACCTCTTATGGCTAAGTCTTTGACTGTGTTTCATTTACCAAG
 1441 TTGACCCAGTTTGTCTTTTAGGTTAAGTAAGAACTCGAGAGTAAAGGCAAGGAGGGGGGC
 1501 CAGCCTCTGAATGCGGCCACGGATGCCTTGCTGCTGCAACCCTTTCCCCAGCTGTCCACT
 1561 GAAACGTGAAGTCTCTGTTTGAATGCCAAACCCACCATTCACTGGTGCTGACTACATAGA
 1621 ATGGGTTGAGAGAAGATCAGTTTGGGCTTCACAGTGTCATTTGAAAAAGCGTTTTTGT
 1681 TGTTTTGAATTATTGTGGAAAACCTTCAAGTGAACAGAAGGATGGTGTCCTACTGTGGAT
 1741 GAGGGATGAACAAGGGGATGGCTTTGATCCAATGGAGCCTGGGAGGTGTGCCAGAAAGC
 1801 TTGTCTGTAGCGGGTTTTGTGAGAGTGAACACTTTCCACTTTTTTGACACCTTATCCTGAT
 1861 GTATGGTTCCAGGATTTGGATTTTGATTTTCCAAATGTAGCTTGAAATTTCAATAAACTT
 1921 TGCTCTGTTTTTCTAAAAATAAAAA

Fig. 13

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.48	0.50	0	1
Marital status	0.65	0.48	0	1
Education	12.5	1.5	9	16
Income	15.2	3.5	10	25
Health status	0.75	0.42	0	1
Smoking status	0.35	0.48	0	1
Alcohol consumption	0.25	0.43	0	1
Exercise frequency	0.15	0.35	0	1
Stress level	0.60	0.45	0	1
Sleep quality	0.55	0.40	0	1
Work satisfaction	0.45	0.50	0	1
Life satisfaction	0.50	0.50	0	1
Depression score	10.5	5.5	0	30
Anxiety score	12.0	6.0	0	35
Quality of life score	75.0	15.0	50	100

Fig. 14

614 GTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCAC..ATCTTGTTCTA 661
 |||||
 640 gtgtaagtggctctgtcctcaggggtgggcagagccactaaacttgtttta 689
 662 CCTAGTTCTTTCCAGTTTGT TTTTGGCTCCCCAAGGGTCATCTCATGTGG 711
 |||||
 690 cctagttctttccagtttg ttttggctccccaagcatcatctcacgagg 739
 712 AGAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATG 761
 |||||
 740 agaactttacacctagcacagctggtgccaaagagatgtcctaaggacatg 789
 762 CCCATCTGGGTCCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCT 811
 |||
 790 gccacctgggtccactccagcgacagacccctgac.aagagcaggtctct 838
 812 GGAGACTAAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTGTCTG 861
 |||||
 839 ggaggctgagttgcatggggcctagtaacaccaagccagtgagcctctaa 888
 862 TGTCACCGGGGCCCTGGGGGCTCCCAGGG.CTGGGCAACTTAGTTACAGCT 910
 ||
 889 tgctactgcgccctgggggctcccagggcctgggcaacttagctgcaact 938
 911 GACCAAGGAGAAAGTAGTTTGTGAGATGTGATGCCAGTGTGCTCCAGAAAG 960
 ||
 939 ggcaaaggagaagggtagtttgaggtgtgacaccagtttgctccagaaag 988
 961 TGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCT 1010
 |
 989 ttttaaggggtctgtttctcatctccatggacatcttcaacagcttcacct 1038
 1011 GACAATGACTGTTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAA 1060
 |||||
 1039 gacaacgactgttcctatgaagaagccacttggtgtttaagcagaggcaa 1088
 1061 CCTCTCTCTTCTTCCCTCTGTCTTTTCCAGGCAGGGG.CAGAGATGGGAGA 1109
 |||||
 1089 cctctctcttc.tcctctgttctcgtaaggcaggggacacagatgggaga 1137
 1110 GATTGAGCCAAATGAGCCTTCTGTTGGTTAATACTGTATAATGCATGGCT 1159
 |||||
 1138 gattgagccaagttagccttctgttggttaatatggtataatgcatggct 1187
 1160 TTGTGCACAGCCCAGTGTGGGGTTACAGCTTTGGGATGACTGCTTATAAA 1209
 |||||
 1188 ttgtgcacagcccagtggtgggattacagctttgggatgaccgcttataaa 1237
 1210 GTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT.AATGCG 1258
 |||||
 1238 gttctgtttggttagtattggcatagtttttctatatagccataaatgcy 1287
 1259 TATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACA 1308
 |||||
 1288 tatatatacccatagggctagatctgtatcttagtgtagcgatgtataca 1337

Fig. 14 (cont)

[illegible]

Fig. 14 (Cont.)

mG 1 MNTEMYQTPMEVAVYQLHNFSTSFSSLLGGDVVSVKLDNSASGASVVAL 50
 hG 1 MNTEMYQTPMEVAVYQLHNFSSISFFSSLLGGDVVSVKLDNSASGASVVAI 50
 =====
 hT 2 KSQWCRPVAMD LGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI 51
 =====

 mG 51 DNKIEQAMD LVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL 100
 hG 51 DNKIEQAMD LVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL 100
 =====
 hT 52 DNKIEQAMD LVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENLLKTL 101
 =====
 hD 1 MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL 41
 =====

 mG 101 ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGS AV* 138
 hG 101 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGS AV* 135
 =====
 hT 102 ASPEQLAQFQAQLQTGSPATTQPGTTQPPAQPASQSGGPTA* 145
 =====
 hD 42 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGS AV*
 =====

Fig. 15